

## SEQUENCE LISTING

&lt;110&gt; Chambon, Pierre - Metzger, Daniel

&lt;120&gt; Transgenic mouse for targeted recombination mediated by modified Cre-ER

&lt;130&gt; D18961

&lt;150&gt; FR 00 12 570

&lt;151&gt; 2000-10-03

&lt;160&gt; 14

&lt;170&gt; PatentIn Ver. 2.1

&lt;210&gt; 1

&lt;211&gt; 1788

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1788)

```

<400> 1
atg acc atg acc ctc cac acc aaa gca tct ggg atg gcc cta ctg cat 48
Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His
      1              5              10              15

cag atc caa ggg aac gag ctg gag ccc ctg aac cgt ccg cag ctc aag 96
Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys
      20              25              30

atc ccc ctg gag cgg ccc ctg ggc gag gtg tac ctg gac agc agc aag 144
Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys
      35              40              45

ccc gcc gtg tac aac tac ccc gag ggc gcc gcc tac gag ttc aac gcc 192
Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
      50              55              60

gcg gcc gcc gcc aac gcg cag gtc tac ggt cag acc ggc ctc ccc tac 240
Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr
      65              70              75              80

ggc ccc ggg tct gag gct gcg gcg ttc ggc tcc aac ggc ctg ggg ggt 288
Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly
      85              90              95

ttc ccc cca ctc aac agc gtg tct ccg agc ccg ctg atg cta ctg cac 336
Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
      100              105              110

ccg ccg ccg cag ctg tcg cct ttc ctg cag ccc cac ggc cag cag gtg 384
Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val
      115              120              125

ccc tac tac ctg gag aac gag ccc agc ggc tac acg gtg cgc gag gcc 432
Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala
      130              135              140

```

ggc ccg ccg gca ttc tac agg cca aat tca gat aat cga cgc cag ggt 480  
 Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly  
 145 150 155 160

ggc aga gaa aga ttg gcc agt acc aat gac aag gga agt atg gct atg 528  
 Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met  
 165 170 175

gaa tct gcc aag gag act cgc tac tgt gca gtg tgc aat gac tat gct 576  
 Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala  
 180 185 190

tca ggc tac cat tat gga gtc tgg tcc tgt gag ggc tgc aag gcc ttc 624  
 Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe  
 195 200 205

ttc aag aga agt att caa gga cat aac gac tat atg tgt cca gcc acc 672  
 Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr  
 210 215 220

aac cag tgc acc att gat aaa aac agg agg aag agc tgc cag gcc tgc 720  
 Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys  
 225 230 235 240

cgg ctg cgc aaa tgc tac gaa gtg gga atg atg aaa ggt ggg ata cga 768  
 Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg  
 245 250 255

aaa gac cga aga gga ggg aga atg ttg aaa cac aag cgc cag aga gat 816  
 Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp  
 260 265 270

gat ggg gag ggc agg ggt gaa gtg ggg tct gct gga gac atg aga gct 864  
 Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala  
 275 280 285

gcc aac ctt tgg cca agc ccg ctg atg atc aaa cgc tct aag aag aac 912  
 Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn  
 290 295 300

agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg ttg 960  
 Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu  
 305 310 315 320

gat gct gag ccc ccc ata ctg tat tcc gag tat gat cct acc aga ccc 1008  
 Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro  
 325 330 335

ttc agt gaa gct tcg atg atg gcc tta ctg acc aac ctg gca gac agg 1056  
 Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg  
 340 345 350

gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca gcc ttt gtg 1104  
 Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val  
 355 360 365

gat ttg acc ctg cat gat cag gtc cac ctt cta gaa tgt gcc tgg cta 1152  
 Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu  
 370 375 380

gag atc ctg atg att ggt ctg gtc tgg cgc tcc atg gag cac cca ggg 1200

3

Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly	385	390	395	400	
aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga aaa	1248				
Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys	405	410	415		
tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca tca	1296				
Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser	420	425	430		
tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc ctc	1344				
Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu	435	440	445		
aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc agc	1392				
Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser	450	455	460		
acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg gac	1440				
Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp	465	470	475	480	
aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg acc	1488				
Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr	485	490	495		
ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc tcc	1536				
Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser	500	505	510		
cac atc agg cac atg agt aac aaa ggc atg gag cat ctg tac agc atg	1584				
His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met	515	520	525		
aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag atg ctg	1632				
Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu	530	535	540		
gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc gtg	1680				
Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val	545	550	555	560	
gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca tcy	1728				
Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser	565	570	575		
cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc cct	1776				
His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro	580	585	590		
gcc aca gtc tga	1788				
Ala Thr Val	595				

<210> 2  
 <211> 595  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 2

Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His  
 1 5 10 15

Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys  
 20 25 30

Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys  
 35 40 45

Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala  
 50 55 60

Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr  
 65 70 75 80

Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly  
 85 90 95

Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His  
 100 105 110

Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Cln Val  
 115 120 125

Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala  
 130 135 140

Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly  
 145 150 155 160

Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met  
 165 170 175

Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala  
 180 185 190

Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe  
 195 200 205

Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr  
 210 215 220

Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys  
 225 230 235 240

Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg  
 245 250 255

Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp  
 260 265 270

Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala  
 275 280 285

Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn  
 290 295 300

Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu  
 305 310 315 320

5

Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro  
 325 330 335  
 Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg  
 340 345 350  
 Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val  
 355 360 365  
 Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu  
 370 375 380  
 Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly  
 385 390 395 400  
 Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys  
 405 410 415  
 Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser  
 420 425 430  
 Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu  
 435 440 445  
 Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser  
 450 455 460  
 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp  
 465 470 475 480  
 Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr  
 485 490 495  
 Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser  
 500 505 510  
 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met  
 515 520 525  
 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu  
 530 535 540  
 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val  
 545 550 555 560  
 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser  
 565 570 575  
 His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro  
 580 585 590  
 Ala Thr Val  
 595

&lt;210&gt; 3

&lt;211&gt; 1983

&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

6

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1983)

&lt;220&gt;

&lt;223&gt; Chimeric sequence Homosapiens-Bacteriophage P1

&lt;400&gt; 3

atg tcc aat tta ctg acc gta cac caa aat ttg cct gca tta ccg gtc	48
Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val	
1 5 10 15	
gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg	96
Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg	
20 25 30	
gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt	144
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val	
35 40 45	
tgc cgg tcg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt	192
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe	
50 55 60	
ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg	240
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala	
65 70 75 80	
cgc ggl ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac	288
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn	
85 90 95	
atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct	336
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala	
100 105 110	
gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt	384
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly	
115 120 125	
gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag	432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln	
130 135 140	
gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat	480
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn	
145 150 155 160	
ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa	528
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu	
165 170 175	
att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga	576
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg	
180 185 190	
atg tta atc cat att gcc aga acg aaa acg ctg gtt agc acc gca ggt	624
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly	
195 200 205	
gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg	672

11/05 2001 VEN 17:18 FAX 01 44 29 35 99 CABINET REGIMBEAU  
 007/023

Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	
210						215					220					
att	tcc	gtc	tct	ggt	gta	gct	gat	gat	cgc	aat	aac	tac	ctg	ttt	tgc	720
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	
225					230					235					240	
cgg	gtc	aga	aaa	aat	ggt	gtt	gcc	gcg	cca	tct	gcc	acc	agc	cag	cta	768
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	
				245					250					255		
tca	act	cgc	gcc	ctg	gaa	ggg	att	ttc	gaa	gca	act	cat	cga	ttg	att	816
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	
			260					265					270			
tac	ggc	gct	aag	gat	gac	tct	ggt	cag	aga	tac	ctg	gcc	tgg	tct	gga	864
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	
		275				280						285				
cac	agt	gcc	cgt	gtc	gga	gcc	gcg	cga	gat	atg	gcc	cgc	gct	gga	gtt	912
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
	290					295					300					
tca	ata	cgc	gag	atc	atg	caa	gct	ggt	ggc	tgg	acc	aat	gta	aat	att	960
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
305					310					315					320	
gtc	atg	aac	tat	atc	cgt	aac	ctg	gat	agt	gaa	aca	ggg	gca	atg	gtg	1008
Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
				325					330					335		
cgc	ctg	ctg	gaa	gat	ggc	gat	ctc	gag	cca	tct	gct	gga	gac	atg	aga	1056
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	
			340					345					350			
gct	gcc	aac	ctt	tgg	cca	agc	cgc	ctc	atg	atc	aaa	cgc	tct	aag	aag	1104
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	
		355				360						365				
aac	agc	ctg	gcc	ttg	tcc	ctg	acg	gcc	gac	cag	atg	gtc	agt	gcc	ttg	1152
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	
	370					375				380						
ttg	gat	gct	gag	ccc	ccc	ata	ctc	tat	tcc	gag	tat	gat	cct	acc	aga	1200
Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	
385					390					395					400	
ccc	ttc	agt	gaa	gct	tgc	atg	atg	ggc	tta	ctg	acc	aac	ctg	gca	gac	1248
Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	
				405					410					415		
agg	gag	ctg	gtt	cac	atg	atc	aac	tgg	gcg	aag	agg	gt				

8

450	455	460	
ggg aag cta ctg ttt got cct aac ttg ctc ttg gac agg aac cag gga			1440
Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly			
465	470	475	480
aaa tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca			1488
Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr			
	485	490	495
tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc			1536
Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys			
	500	505	510
ctc aaa tot att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc			1584
Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser			
	515	520	525
agc acc ctg aag tot ctg gaa gag aag gac cat atc cac cga gtc ctg			1632
Ser Thr Leu Lys Ser Leu Glu Lys Asp His Ile His Arg Val Leu			
	530	535	540
gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg			1680
Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu			
	545	550	555
acc ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc			1728
Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu			
	565	570	575
tcc cac atc agg cac atg agt aac aaa aga atg gag cat ctg tac agc			1776
Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu His Leu Tyr Ser			
	580	585	590
atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag atg			1824
Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met			
	595	600	605
ctg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc			1872
Leu Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser			
	610	615	620
gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca			1920
Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser			
	625	630	635
tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc			1968
Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe			
	645	650	655
cct gcc aca gtc tga			1983
Pro Ala Thr Val			
	660		

&lt;210&gt; 4

&lt;211&gt; 660

&lt;212&gt; PRT

&lt;213&gt; Artificial sequence

&lt;223&gt; Chimeric sequence Homosapiens-Bacteriophage P1



&lt;400&gt; 4

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val  
 1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg  
 20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
 85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln  
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg  
 180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp  
 210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
 225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu  
 245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly  
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
 290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile  
 305 310 315 320

10

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
 325 330 335  
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg  
 340 345 350  
 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys  
 355 360 365  
 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu  
 370 375 380  
 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg  
 385 390 395 400  
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp  
 405 410 415  
 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe  
 420 425 430  
 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp  
 435 440 445  
 Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro  
 450 455 460  
 Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly  
 465 470 475 480  
 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr  
 485 490 495  
 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys  
 500 505 510  
 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser  
 515 520 525  
 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu  
 530 535 540  
 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu  
 545 550 555 560  
 Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu  
 565 570 575  
 Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu His Leu Tyr Ser  
 580 585 590  
 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met  
 595 600 605  
 Leu Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser  
 610 615 620  
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser  
 625 630 635 640  
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe

```
<210> 5
<211> 1983
<212> DNA
<213> Artificial sequence
```

<220>  
<221> CDS  
<222> (1)..(1983)

<220>  
<223> Chimeric sequence Homosapiens-Bacteriophage P1

[illegible]

12

Leu Ala Phe	Leu Gly Ile Ala Tyr Asn Thr	Leu Leu Arg Ile Ala Glu	
	165	170 175	
att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga	576		
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg			
	180 185 190		
atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt	624		
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly			
	195 200 205		
gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg	672		
Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp			
	210 215 220		
att tcc gtc tct ggt gta gct gat gat ccg aat aac tac ctg ttt tgc	720		
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys			
	225 230 235 240		
cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta	768		
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu			
	245 250 255		
tca act cgc gcc ctg gaa ggg att ttt gaa gca act cat cga ttg att	816		
Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile			
	260 265 270		
tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga	864		
Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly			
	275 280 285		
cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt	912		
His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val			
	290 295 300		
tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att	960		
Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile			
	305 310 315 320		
gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg	1008		
Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val			
	325 330 335		
cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga	1056		
Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg			
	340 345 350		
gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag	1104		
Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys			
	355 360 365		
aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg	1152		
Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu			
	370 375 380		
ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga	1200		
Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg			
	385 390 395 400		
ccc ttc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac	1248		
Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp			

405										410					415					
agg	gag	ctg	gtt	cac	atg	atc	aac	tgg	gcg	aag	agg	gtg	cca	ggc	ttt		1296			
Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe					
420										425					430					
gtg	gat	ttg	acc	ctc	cat	gat	cag	gtc	cac	ctt	cta	gaa	tgt	gcc	ttg		1344			
Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp					
435										440					445					
cta	gag	atc	ctg	atg	att	ggt	ctc	gtc	tgg	cgc	tcc	atg	gag	cac	cca		1392			
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro					
450										455					460					
gtg	aag	cta	ctg	ttt	gct	cct	aac	ttg	ctc	ttg	gac	agg	aac	cag	gga		1440			
Val	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly					
465										470					475					480
aaa	tgt	gta	gag	ggc	atg	gtg	gag	atc	ttc	gac	atg	ctg	ctg	gct	aca		1488			
Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr					
485										490					495					
tca	tct	cgg	ttc	cgc	atg	atg	aat	ctg	cag	gga	gag	gag	ttt	gtg	tgc		1536			
Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys					
500										505					510					
ctc	aaa	tct	att	att	ttg	ctt	aat	tct	gga	gtg	tac	aca	ttt	ctg	tcc		1584			
Leu	Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val	Tyr	Thr	Phe	Leu	Ser					
515										520					525					
agc	acc	ctg	aag	tct	ctg	gaa	gag	aag	gac	cat	atc	cac	cga	gtc	ctg		1632			
Ser	Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His	Ile	His	Arg	Val	Leu					
530										535					540					
gac	aag	atc	aca	gac	act	ttg	atc	cac	ctg	atg	gcc	aag	gca	ggc	ctg		1680			
Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met	Ala	Lys	Ala	Gly	Leu					
545										550					555					560
acc	ctg	cag	cag	cag	cac	cag	cgg	ctg	gcc	cag	ctc	ctc	ctc	atc	ctc		1728			
Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu					
565										570					575					
tcc	cac	atc	agg	cac	atg	agt	aac	aaa	ggc	atg	gag	cat	ctg	tac	agc		1776			
Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser					
580										585					590					
atg	aag	tgc	aag	aac	gtg	gtg	ccc	ctc	tat	gac	ctg	ctg	ctg	gag	gcg		1824			
Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Leu	Tyr	Asp	Leu	Leu	Leu	Glu	Ala					
595										600					605					
gcg	gac	gcc	cac	cgc	cta	cat	gcg	ccc	act	agc	cgt	gga	ggg	gca	tcc		1872			
Ala	Asp	Ala	His	Arg	Leu	His	Ala	Pro	Thr	Ser	Arg	Gly	Gly	Ala	Ser					
610										615					620					
gtg	gag	gag	acg	gac	caa	agc	cac	ttg	gcc	act	gcg	ggc	tct	act	tca		1920			
Val	Glu	Glu	Thr	Asp	Gln	Ser	His	Leu	Ala	Thr	Ala	Gly	Ser	Thr	Ser					
625										630					635					640
tcg	cat	tcc	ttg	caa	aag	tat	tac	atc	acg	ggg	gag	gca	gag	ggt	ttc		1968			
Ser	His	Ser	Leu	Gln	Lys	Tyr	Tyr	Ile	Thr	Gly	Glu	Ala	Glu	Gly	Phe					
645										650					655					

14

cct gcc aca gct tga  
Pro Ala Thr Ala  
660

1983

<210> 6  
<211> 660  
<212> PRT  
<213> Artificial sequence  
<223> Chimeric sequence Homosapiens-Bacteriophage P1

<400> 6  
Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val  
1 5 10 15  
Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg  
20 25 30  
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
35 40 45  
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
50 55 60  
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
65 70 75 80  
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
85 90 95  
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
100 105 110  
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
115 120 125  
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln  
130 135 140  
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
145 150 155 160  
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
165 170 175  
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg  
180 185 190  
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
195 200 205  
Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp  
210 215 220  
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
225 230 235 240  
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu  
245 250 255

15

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
 260 265 270  
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly  
 275 280 285  
 His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
 290 295 300  
 Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile  
 305 310 315 320  
 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
 325 330 335  
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg  
 340 345 350  
 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys  
 355 360 365  
 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu  
 370 375 380  
 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg  
 385 390 395 400  
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp  
 405 410 415  
 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe  
 420 425 430  
 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp  
 435 440 445  
 Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro  
 450 455 460  
 Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly  
 465 470 475 480  
 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr  
 485 490 495  
 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys  
 500 505 510  
 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser  
 515 520 525  
 Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu  
 530 535 540  
 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu  
 545 550 555 560  
 Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu  
 565 570 575  
 Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser

<400> 7																	
atg	tcc	aat	tta	ctg	acc	gta	cac	caa	aat	ttg	cct	gca	tta	ccg	gtc	48	
Met	Ser	Asn	Leu	Leu	Thr	Val	His	Gln	Asn	Leu	Pro	Ala	Leu	Pro	Val		
1				5					10					15			
gat	gca	acg	agt	gat	gag	gtt	cgc	aag	aac	ctg	atg	gac	atg	ttc	agg	96	
Asp	Ala	Thr	Ser	Asp	Glu	Val	Arg	Lys	Asn	Leu	Met	Asp	Met	Phe	Arg		
			20					25					30				
gat	cgc	cag	gcg	ttt	tct	gag	cat	acc	tgg	aaa	atg	ctt	ctg	tcc	gtt	144	
Asp	Arg	Gln	Ala	Phe	Ser	Glu	His	Thr	Trp	Lys	Met	Leu	Leu	Ser	Val		
		35				40						45					
tgc	cgg	tcg	tgg	gcg	gca	tgg	tgc	aag	ttg	aat	aac	cgg	aaa	tgg	ttt	192	
Cys	Arg	Ser	Trp	Ala	Ala	Trp	Cys	Lys	Leu	Asn	Asn	Arg	Lys	Trp	Phe		
	50					55					60						
ccc	gca	gaa	cct	gaa	gat	gtt	cgc	gat	tat	ctt	cta	tat	ctt	cag	gcg	240	
Pro	Ala	Glu	Pro	Glu	Asp	Val	Arg	Asp	Tyr	Leu	Leu	Tyr	Leu	Gln	Ala		
65					70					75				80			
cgc	ggt	ctg	gca	gta	aaa	act	atc	cag	caa	cat	ttg	ggc	cag	cta	aac	288	
Arg	Gly	Leu	Ala	Val	Lys	Thr	Ile	Gln	Gln	His	Leu	Gly	Gln	Leu	Asn		
				85					90				95				
atg	ctt	cat	cgt	cgg	tcc	ggg	ctg	cca	cga	cca	agt	gac	agc	aat	gct	336	
Met	Leu	His	Arg	Arg	Ser	Gly	Leu	Pro	Arg	Pro	Ser	Asp	Ser	Asn	Ala		
			100					105					110				
gtt	tca	ctg	gtt	atg	cgg	cgg	atc	cga	aaa	gaa	aac	gtt	gat	gcc	ggg	384	



17

Val	Ser	Leu	Val	Met	Arg	Arg	Ile	Arg	Lys	Glu	Asn	Val	Asp	Ala	Gly		
		115					120					125					
gaa	cgt	gca	aaa	cag	gct	cta	gcg	ttc	gaa	cgc	act	gat	ttc	gac	cag	432	
Glu	Arg	Ala	Lys	Gln	Ala	Leu	Ala	Phe	Glu	Arg	Thr	Asp	Phe	Asp	Gln		
	130					135					140						
gtt	cgt	tca	ctc	atg	gaa	aat	agc	gat	cgc	tgc	cag	gat	ata	cgt	aat	480	
Val	Arg	Ser	Leu	Met	Glu	Asn	Ser	Asp	Arg	Cys	Gln	Asp	Ile	Arg	Asn		
	145				150					155					160		
ctg	gca	ttt	ctg	ggg	att	gct	tat	aac	acc	ctg	tta	cgt	ata	gcc	gaa	528	
Leu	Ala	Phe	Leu	Gly	Ile	Ala	Tyr	Asn	Thr	Leu	Leu	Arg	Ile	Ala	Glu		
			165					170						175			
att	gcc	agg	atc	agg	gtt	aaa	gat	atc	tca	cgt	act	gac	ggt	ggg	aga	576	
Ile	Ala	Arg	Ile	Arg	Val	Lys	Asp	Ile	Ser	Arg	Thr	Asp	Gly	Gly	Arg		
		180						185					190				
atg	tta	atc	cat	att	ggc	aga	acg	aaa	acg	ctg	gtt	agc	acc	gca	ggt	624	
Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly		
	195					200						205					
gta	gag	aag	gca	ctt	agc	ctg	ggg	gta	act	aaa	ctg	gtc	gag	cga	tgg	672	
Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp		
	210					215					220						
att	tcc	gtc	tct	ggt	gta	gct	gat	gat	ccg	aat	aac	tac	ctg	ttt	tgc	720	
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys		
	225				230					235					240		
cgg	gtc	aga	aaa	aat	ggt	gtt	gcc	gcg	cca	tct	gcc	acc	agc	cag	cta	768	
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu		
			245						250					255			
tca	act	cgc	gcc	ctg	gaa	ggg	att	ttt	gaa	gca	act	cat	cga	ttg	att	816	
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile		
			260					265					270				
tac	ggc	gct	aag	gat	gac	tct	ggt	cag	aga	tac	ctg	gcc	tgg	tct	gga	864	
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly		
	275					280					285						
cac	agt	gcc	cgt	gtc	gga	gcc	gcg	cga	gat	atg	gcc	cgc	gct	gga	gtt	912	
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val		
	290					295					300						
tca	ata	ccg	gag	atc	atg	caa	gct	ggt	ggc	tgg	acc	aat	gta	aat	att	960	
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile		
	305				310					315					320		
gtc	atg	aac	tat	atc	cgt	aac	ctg	gat	agt	gaa	aca	ggg	gca	atg	gtg	1008	
Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val		
			325					330					335				
cgc	ctg	ctg	gaa	gat	ggc	gat	ctc	gag	cca	tct	gct	gga	gac	atg	aga	1056	
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg		
			340					345					350				
gct	gcc	aac	ctt	tgg	cca	agc	ccg	ctc	atg	atc	aaa	cgc	tct	aag	aag	1104	
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys		

355				360				365								
aac	agc	ctg	gcc	ttg	tcc	ctg	acg	gcc	gac	cag	atg	gtc	agt	gcc	ttg	1152
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	
370				375				380								
ttg	gat	gct	gag	ccc	ccc	ata	ctc	tat	tcc	gag	tat	gat	cct	acc	aga	1200
Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	
385				390				395				400				
ccc	ttc	agt	gaa	gct	tcg	atg	atg	ggc	tta	ctg	acc	aac	ctg	gca	gac	1248
Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	
405				410				415								
agg	gag	ctg	gtt	cac	atg	atc	aac	tgg	gcg	aag	agg	gtg	cca	ggc	ttt	1296
Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	
420				425				430								
gtg	gat	ttg	acc	ctc	cat	gat	cag	gtc	cac	ctt	cta	gaa	tgt	gcc	tgg	1344
Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	
435				440				445								
cta	gag	atc	ctg	atg	att	ggc	ctc	gtc	tgg	cgc	tcc	atg	gag	cac	cca	1392
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro	
450				455				460								
ggg	aag	cta	ctg	ttt	gct	cct	aac	ttg	ctc	ttg	gac	agg	aac	cag	gga	1440
Gly	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly	
465				470				475				480				
aaa	tgt	gta	gag	ggc	atg	gtg	gag	atc	ttc	gac	atg	ctg	ctg	gct	aca	1488
Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	
485				490				495								
tca	tct	cgg	ttc	cgc	atg	atg	aat	ctg	cag	gga	gag	gag	ttt	gtg	tgc	1536
Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys	
500				505				510								
ctc	aaa	tct	att	att	ttg	ctt	aat	tct	gga	gtg	tac	aca	ttt	ctg	tcc	1584
Leu	Lys	Ser	Ile	Ile	Leu	Leu	Asn	Ser	Gly	Val	Tyr	Thr	Phe	Leu	Ser	
515				520				525								
agc	acc	ctg	aag	tct	ctg	gaa	gag	aag	gac	cat	atc	cac	cga	gtc	ctg	1632
Ser	Thr	Leu	Lys	Ser	Leu	Glu	Glu	Lys	Asp	His	Ile	His	Arg	Val	Leu	
530				535				540								
gac	aag	atc	aca	gac	act	ttg	atc	cac	ctg	atg	gcc	aag	gca	ggc	ctg	1680
Asp	Lys	Ile	Thr	Asp	Thr	Leu	Ile	His	Leu	Met	Ala	Lys	Ala	Gly	Leu	
545				550				555				560				
acc	ctg	cag	cag	cag	cac	cag	cgg	ctg	gcc	cag	ctc	ctc	ctc	atc	ctc	1728
Thr	Leu	Gln	Gln	Gln	His	Gln	Arg	Leu	Ala	Gln	Leu	Leu	Leu	Ile	Leu	
565				570				575								
tcc	cac	atc	agg	cac	atg	agt	aac	aaa	ggc	atg	gag	cat	ctg	tac	agc	1776
Ser	His	Ile	Arg	His	Met	Ser	Asn	Lys	Gly	Met	Glu	His	Leu	Tyr	Ser	
580				585				590								
atg	aag															

gcg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc 1872  
Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser  
610 615 620

gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca 1920  
Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser  
625 630 635 640

tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc 1968  
Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe  
645 650 655

cct gcc aca gct tga 1983  
Pro Ala Thr Ala  
660

<210> 日

<211> 660

<212> PRT

<213> Artificial sequence

<223> Chimeric sequence Homosapiens-Bacteriophage P1

<400> 8

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val  
1 5 10 15

Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg  
20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val  
35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe  
50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala  
65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn  
85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala  
100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly  
115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln  
130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn  
145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu  
165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg  
180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly  
195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp  
210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys  
225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu  
245 250 255

Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile  
260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly  
275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val  
290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile  
305 310 315 320

Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val  
325 330 335

Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg  
340 345 350

Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys  
355 360 365

Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu  
370 375 380

Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg  
385 390 395 400

Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp  
405 410 415

Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe  
420 425 430

Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp  
435 440 445

Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro  
450 455 460

Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly  
465 470 475 480

Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr  
485 490 495

Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys  
500 505 510

Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser

```

<210> 9
<211> 20
<212> DNA
<213> Homo sapiens

<400> 9
tccttcacca agcaaatctg 20

<210> 10
<211> 20
<212> DNA
<213> Homo sapiens

<400> 10
tgcagccctc acaactgtat 20

<210> 11
<211> 21
<212> DNA
<213> Homo sapiens

<400> 11
caacctgcac ttgtcactta g 21

<210> 12
<211> 20
<212> DNA

```

22

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

atgtttcata gttggatatac

20

&lt;210&gt; 13

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 13

atacgcggcc gcgaattcca gcaggaatca ggtagct

37

&lt;210&gt; 14

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;400&gt; 14

atagcgccgg cgctgcagca caggagggtg ctatgag

37